

*re-run*

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/536,935A  
Source: FW  
Date Processed by STIC: 6/8/06

# ***ENTERED***



## RAW SEQUENCE LISTING

DATE: 08/08/2006

PATENT APPLICATION: US/10/536,935A

TIME: 18:09:06

Input Set : N:\Crf4\Refhold\10\_folder\J536935A.raw

Output Set: N:\CRF4\08082006\J536935A.raw

1 <110> APPLICANT: Tsukahara, Kappei  
 2 Tsuchiya, Mamiko  
 3 Jigami, Yoshifumi  
 4 Nakayama, Kenichi  
 5 Umemura, Mariko  
 6 Okamoto, Michiyo  
 7 <120> TITLE OF INVENTION: METHOD OF SCREENING FOR COMPOUNDS THAT  
 8 INHIBIT THE ENZYMATIC ACTIVITY OF GWT1 GENE PRODUCT  
 9 <130> FILE REFERENCE: 082368-004400US  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/536,935A  
 11 <141> CURRENT FILING DATE: 2005-05-20  
 12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/14909  
 13 <151> PRIOR FILING DATE: 2003-11-21  
 14 <150> PRIOR APPLICATION NUMBER: JP 2002-339418  
 15 <151> PRIOR FILING DATE: 2002-11-22  
 16 <160> NUMBER OF SEQ ID NOS: 18  
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 1497  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Saccharomyces cerevisiae  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: (1)..(1494)  
 25 <400> SEQUENCE: 1  
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 27 atg gca aca gta cat cag aag aat atg tcg act tta aaa cag aga aaa 48  
 28 Met Ala Thr Val His Gln Lys Asn Met Ser Thr Leu Lys Gln Arg Lys  
 29 1 5 10 15  
 30 gag gac ttt gtg aca ggg ctc aat ggc ggt tct ata aca gaa att aac 96  
 31 Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn  
 32 20 25 30  
 33 gca gtg aca tca att gct ttg gta act tac ata tca tgg aac tta ttg 144  
 34 Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu  
 35 35 40 45  
 36 aaa aat tcc aac ctt atg cct cct ggc att tcc agc gtg caa tac ata 192  
 37 Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile  
 38 50 55 60  
 39 att gat ttt gca ttg aac tgg gtt gct ttg ctt cta tct att act att 240  
 40 Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Leu Ser Ile Thr Ile  
 41 65 70 75 80  
 42 tat gct agt gaa cca tac ctt cta aac acg cta ata ctg tta cct tgt 288  
 43 Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys  
 44 85 90 95

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45	ttg ctc gca ttc ata tat gga aaa ttt act agc tcg agt aaa cct tct	336
46	Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Ser Lys Pro Ser	
47	100 105 110	
48	aat cca ata tac aat aaa aaa aaa atg att aca cag cgg ttc caa cta	384
49	Asn Pro Ile Tyr Asn Lys Lys Lys Met Ile Thr Gln Arg Phe Gln Leu	
50	115 120 125	
51	gaa aaa aag ccg tat att act gcg tat cgt ggt ggg atg ctt att ctg	432
52	Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu	
53	130 135 140	
54	act gct att gcc atc ttg gct gta gat ttt cca att ttc cca agg agg	480
55	Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg	
56	145 150 155 160	
57	ttt gcc aag gtg gaa act tgg ggg aca tcc ctg atg gat ctt ggt gta	528
58	Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val	
59	165 170 175	
60	gga tca ttc gtt ttc agt aac ggt att gtt tct tct agg gca ctg ttg	576
61	Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu	
62	180 185 190	
63	aaa aac cta agc ttg aag agt aaa ccc agc ttc tta aaa aat gca ttt	624
64	Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe	
65	195 200 205	
66	aat gcc tta aaa tca gga gga act cta ttg ttc cta gga ttg ctg agg	672
67	Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg	
68	210 215 220	
69	ttg ttt ttt gta aaa aat ttg gaa tat caa gaa cat gtc aca gaa tat	720
70	Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr	
71	225 230 235 240	
72	ggg gtt cat tgg aat ttt ttt atc acc cta tca ttg ttg cca ctt gta	768
73	Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val	
74	245 250 255	
75	ttg acc ttt att gat ccc gtc aca aga atg gtt cca cgc tgc tca att	816
76	Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile	
77	260 265 270	
78	gca ata ttc att tca tgc att tat gaa tgg cta ctt tta aag gac gat	864
79	Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Leu Lys Asp Asp	
80	275 280 285	
81	cgc act tta aac ttt tta att ttg gct gat aga aat tgt ttc ttc agt	912
82	Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser	
83	290 295 300	
84	gct aat aga gaa ggc atc ttc tca ttt cta ggt tat tgc tcg att ttt	960
85	Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe	
86	305 310 315 320	
87	ctt tgg ggc caa aac acg gga ttt tac ttg ttg gga aat aaa cca act	1008
88	Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr	
89	325 330 335	
90	tta aac aat ctt tat aag cct tct acg caa gac gta gtt gca gca tca	1056
91	Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser	
92	340 345 350	
93	aag aag tct tcg act tgg gac tat tgg act tca gta acc cca tta agt	1104

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Output Set: N:\CRF4\08082006\J536935A.raw

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94   Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser
95           355           360           365
96   ggc ctc tgt ata tgg agt aca att ttt ctt gtt atc agc cag ttg gtt   1152
97   Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val
98           370           375           380
99   ttt caa tac cat cct tat agt gtt tca aga agg ttt gct aac tta cca   1200
100   Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro
101   385           390           395           400
102   tat act ttg tgg gtc att act tat aat tta cta ttt ttg act ggg tac   1248
103   Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr
104           405           410           415
105   tgc ttg act gac aaa att ttc ggt aat tct tcg gaa tat tat aaa gtt   1296
106   Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val
107           420           425           430
108   gcc gaa tgc ttg gaa tca atc aac tcc aat ggg ttg ttt tta ttt ttg   1344
109   Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu
110           435           440           445
111   ttg gca aat gtc tct act ggt tta gtc aat atg tct atg gtc acg ata   1392
112   Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile
113           450           455           460
114   gat tct tca ccc tta aaa tca ttc ctg gtt ttg ttg gca tac tgc tca   1440
115   Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser
116           465           470           475           480
117   ttc ata gct gtc ata tcg gtt ttc ttg tat aga aaa aga ata ttc att   1488
118   Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile
119           485           490           495
120   aag cta taa   1497
121   Lys Leu
123 <210> SEQ ID NO: 2
124 <211> LENGTH: 498
125 <212> TYPE: PRT
126 <213> ORGANISM: Saccharomyces cerevisiae
127 <400> SEQUENCE: 2
128   Met Ala Thr Val His Gln Lys Asn Met Ser Thr Leu Lys Gln Arg Lys
129       1           5           10           15
130   Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn
131           20           25           30
132   Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu
133           35           40           45
134   Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile
135           50           55           60
136   Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Leu Ser Ile Thr Ile
137           65           70           75           80
138   Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys
139           85           90           95
140   Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Ser Lys Pro Ser
141           100          105          110
142   Asn Pro Ile Tyr Asn Lys Lys Lys Met Ile Thr Gln Arg Phe Gln Leu
143           115          120          125

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Input Set : N:\Crf4\Refhold\10\_folder\J536935A.raw

Output Set: N:\CRF4\08082006\J536935A.raw

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144   Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu
145           130           135           140
146   Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg
147   145           150           155           160
148   Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val
149           165           170           175
150   Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu
151           180           185           190
152   Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe
153           195           200           205
154   Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg
155           210           215           220
156   Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr
157   225           230           235           240
158   Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val
159           245           250           255
160   Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile
161           260           265           270
162   Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Leu Lys Asp Asp
163           275           280           285
164   Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser
165   290           295           300
166   Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe
167   305           310           315           320
168   Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr
169           325           330           335
170   Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser
171           340           345           350
172   Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser
173           355           360           365
174   Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val
175           370           375           380
176   Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro
177   385           390           395           400
178   Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr
179           405           410           415
180   Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val
181           420           425           430
182   Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu
183           435           440           445
184   Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile
185           450           455           460
186   Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser
187   465           470           475           480
188   Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile
189           485           490           495
190   Lys Leu
192 <210> SEQ ID NO: 3
193 <211> LENGTH: 1458

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## RAW SEQUENCE LISTING

DATE: 08/08/2006

PATENT APPLICATION: US/10/536,935A

TIME: 18:09:06

Input Set : N:\Cr4\Refhold\10\_folder\J536935A.raw

Output Set: N:\CRF4\08082006\J536935A.raw

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194 <212> TYPE: DNA
195 <213> ORGANISM: Candida albicans
196 <220> FEATURE:
197 <221> NAME/KEY: CDS
198 <222> LOCATION: (1)..(1455)
199 <400> SEQUENCE: 3
200   atg tca tcg tct tta aaa caa ttg aaa gaa caa ttt gtc tca gat ttg      48
201   Met Ser Ser Ser Leu Lys Gln Leu Lys Glu Gln Phe Val Ser Asp Leu
202       1               5               10               15
203   act ggt ggc aca att gaa gaa att tat gct gta acc agt ata gca tta      96
204   Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu
205               20               25               30
206   tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta     144
207   Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu
208               35               40               45
209   gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc     192
210   Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
211       50               55               60
212   att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt     240
213   Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val
214       65               70               75               80
215   att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca     288
216   Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
217               85               90               95
218   tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa     336
219   Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu
220               100              105              110
221   cta ttg ccg aga aaa caa ttt ata aca gcc tat cgt tct caa atg ttg     384
222   Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu
223               115              120              125
224   ata att act aat cta gct ata tta gct gtt gat ttt cct att ttc cca     432
225   Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro
226       130              135              140
227   aga aga ttt gcc aaa gtg gaa aca tgg ggc acg tca atg atg gat tta     480
228   Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu
229       145              150              155              160
230   gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa     528
231   Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln
232               165              170              175
233   ttg atc aag aac cac acc gac aac tac aaa ttt agt tgg aag agt tat     576
234   Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr
235               180              185              190
236   ttg aaa aca atc aag cag aac ttt atc aag tca gtg cct ata ctt gtt     624
237   Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val
238               195              200              205
239   tta gga gct att cgt ttt gtt agt gtt aag caa ttg gac tat cag gaa     672
240   Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu
241       210              215              220
242   cac gaa aca gag tat gga atc cat tgg aat ttt ttc ttc aca tta ggg     720

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## VERIFICATION SUMMARY

DATE: 08/08/2006

PATENT APPLICATION: US/10/536,935A

TIME: 18:09:07

Input Set : N:\Crf4\Refhold\10\_folder\J536935A.raw

Output Set: N:\CRF4\08082006\J536935A.raw

L:10 M:270 C: Current Application Number differs, Wrong Format

L:1009 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS  
LOCATION:44..2001L:1012 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS  
LOCATION:44..2001L:1057 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS  
LOCATION:44..2001L:1060 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS  
LOCATION:44..2001L:1102 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS  
LOCATION:44..2001L:1105 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS  
LOCATION:44..2001